SEQUENCE LISTING

Sequence Listing
<110> Nara Institute of Science, Technology, Research Institute of Innovative Technology
for the Earth and Kinki University
<120> Transgenic plants
<130> C01F1576
<160> 17
<210> 1
<211> 358
<212> PRT
<213> Spinacia oleracea L
<220> Fructose-1,6-bisphosphatase
<223>
<400> 1

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Lys Tyr Glu Ile Glu Thr Leu Thr Gly Trp Leu Leu Lys Gln Glu Met
                20                  25                  30
Ala Gly Val Ile Asp Ala Glu Leu Thr Ile Val Leu Ser Ser Ile Ser
                35                  40                  45
Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser
    50                  55                  60
Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln
65                  70                  75                  80
Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg
                85                  90                  95
Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro
                100                 105                 110
Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp
                115                 120                 125
Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser
    130                 135                 140
Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp
145                 150                 155                 160
His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val
                165                 170                 175
Asn Val Cys Gln Pro Gly Asp Asn Leu Leu Ala Ala Gly Tyr Cys Met
                180                 185                 190
Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr
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            195                    200                    205
Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu
            210                    225                    220
Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly
225                    230                    235                    240
Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu
                245                    250                    255
Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly
                260                    265                    270
Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr
                275                    280                    285
Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu
            290                    295                    300
Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys
305                    310                    315                    320
Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile
                325                    330                    335
His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys
                340                    345                    350
Leu Glu Lys Tyr Leu Ala
            355
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<210> 2

<211> 1074

<212> DNA

<213> Spinacia oleracea L

<220> Fructose-1,6-bisphosphatase

<223>

<400> 2

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accatcgttc tttctagcat ttcattggct tgtaaacaaa ttgcttcctt ggttcaacga    180
gctggtattt ctaacttgac tggaattcaa ggtgctgtca atatccaagg agaggatcag    240
aagaaacttg atgttgtctc caatgaggtg ttttcgagct gcttgagatc gagtggaaga    300
acaggaataa tagcatcaga agaagaggat gtaccagtgg cagtggaaga gagttactct    360
ggaaactata ttgttgtgtt tgatccactt gatggttcat ccaacattga tgcagctgtc    420
tccactggtt ccatctttgg catttatagc cctaacgatg agtgcattgt tgactctgat    480
cacgacgatg agtcacagct aagtgcagaa gaacagaggt gtgtagtgaa tgtatgtcaa    540
ccaggggata acctattagc agcagggtat tgtatgtact caagctctgt tatcttcgta    600
cttacaattg gtaaaggtgt gtatgcattc acattagatc caatgtatgg tgaattcgta    660
ctcacttcag agaaaatcca aatcccaaaa gctgggaaga tctattcatt caatgaaggt    720
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aactacaaaa tgtgggatga taaattgaag aagtacatgg atgatcttaa agagccagga        780
gagtcacaga aaccgtactc gtctcgttac atagggagtt tagttgggga ctttcataga        840
acactttat atggtgggat ttatggttac ccaagagatg caaagagtaa gaatgggaaa        900
ttgaggcttt tgtatgaatg tgcacctatg agttttattg ttgaacaagc tggtggtaaa        960
ggttctgatg gtcatcaaag aattcttgac attcaaccca ccgagataca tcaacgtgtg        1020
ccactgtaca tcgggagtgt ggaggaagta gagaaattag agaagtactt agca             1074
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<210> 3

<211> 333

<212> PRT

<213> Spinacia oleracea L

<220> Sedoheptulose-1,7-bisphosphatase

<223>

<400> 3

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                   20                  25                  30
Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe
                   35                  40                  45
Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe
       50                  55                  60
Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe
65                  70                  75                  80
Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu
                   85                  90                  95
Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser
                  100                 105                 110
Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe
                  115                 120                 125
Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly
       130                 135                 140
Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro
145                 150                 155                 160
Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu
                  165                 170                 175
Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr
                  180                 185                 190
Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr
                  195                 200                 205
Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu
```

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              210                 215                 220
Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln
225                 230                 235                 240
Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr
                    245                 250                 255
Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe
                260                 265                 270
Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val
                275                 280                 285
Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr
                290                 295                 300
Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser
305                 310                 315                 320
Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala
                    325                 330
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<210> 4
<211> 999
<212> DNA
<213> Spinacia oleracea L
<220> Sedoheptulose-1,7-bisphosphatase
<223>
<400> 4

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gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggtgg aactcaatgt   180
gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttcttttc   240
gaggcattga actattcaca cttctgcaag tatgcttgtt cagaagaact ccctgagctt   300
caagatatgg gaggccccgt tgatggcgga ttcagtgtag catttgaccc ccttgatgga   360
tccagcattg tcgataccaa tttctcagtt gggaccatat cggggtttg gccaggtgac   420
aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttatggtcct   480
aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttcttctt   540
gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc   600
tgtcctggaa acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac   660
tatataaaag agaaatacac attgagatac actggaggaa tggttcctga tgttaaccag   720
atcatagtga aggagaaagg tatattcaca aatgtaatat cacctacagc caaggcaaag   780
ttgaggttac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tggtggtcac   840
agcagtgagg gaaccaagtc tgtgttggac attgaagtca aaaaccttga tgacagaacc   900
caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc   960
tctaggctag aggagccagt tcctgttgga gctgctgct                         999
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<210> 5

<211> 356
<212> PRT
<213> Synechococcus
<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus
PCC 7942
<223>
<400> 5
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Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala
              5                   10                  15
Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala
              20                  25                  30
Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu
              35                  40                  45
Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro
     50                  55                  60
Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys
65                  70                  75                  80
Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val
              85                  90                  95
Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser
              100                 105                 110
Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro
              115                 120                 125
Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys
              130                 135                 140
Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu
145                 150                 155                 160
Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg
              165                 170                 175
Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg
              180                 185                 190
Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly
              195                 200                 205
Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro
     210                 215                 220
Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe
225                 230                 235                 240
Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile
              245                 250                 255
Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile
```

```
        260                265                    270
Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln
            275                280                285
Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu
            290                295                300
Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile
305                310                315                    320
Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe
                325                330                    335
Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp
                340                345                350
Arg Pro Glu Arg
            355
```

<210> 6
<211> 1350
<212> DNA
<213> Synechococcus
<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus PCC.7942
<400> 6

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cgagattatt gaagttgtcg agcaggcagc gatcgcctcg gcccgcctga tgggcaaagg     180
cgaaaagaat gaagccgatc gcgtcgcagt agaagcgatg cgggtgcgga tgaaccaagt     240
ggaaatgctg ggccgcatcg tcatcggtga aggcgagcgc gacgaagcac cgatgctcta     300
tatcggtgaa gaagtgggca tctaccgcga tgcagacaag cgggctggcg taccggctgg     360
caagctggtg gaaatcgaca tcgccgttga cccctgcgaa ggcaccaacc tctgcgccta     420
cggtcagccc ggctcgatgg cagttttggc catctccgag aaaggcggcc tgtttgcagc     480
tcccgacttc tacatgaaga aactggctgc accccccagct gccaaaggca aagagacatc     540
aataaagtcc gcgaccgaaa acctgaaaat tctctcggaa tgtctcgatc gcgccatcga     600
tgaattggtg gtcgtggtca tggatcgtcc ccgccacaaa gagctaatcc aagagatccg     660
ccaagcgggt gcccgcgtcc gtctgatcag cgatggtgac gtttcggccg cgatctcctg     720
cggttttgct ggcaccaaca cccacgccct gatgggcatc ggtgcagctc ccgagggtgt     780
gattcggca gcagcaatgc gttgcctcgg cgggcacttc caaggccagc tgatctacga     840
cccagaagtg gtcaaaaccg gcctgatcgg tgaaagccgt gagagcaaca tcgctcgcct     900
gcaagaaatg ggcatcaccg atcccgatcg tgtctacgac gcgaacgaac tggcttcggg     960
tcaagaagtg ctgtttgcgg cttgcggtat caccccgggc ttgctgatgg aaggcgtgcg    1020
cttcttcaaa ggcggcgctc gcacccagag cttggtgatc tccagccagt cacggacggc    1080
tcgcttcgtt gacaccgttc acatgttcga cgatgtcaaa acggttagcc tgccgttaat    1140
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tcctgatccc aaatggcggc cggagcggta gaacgggtat agctcgatcg cttcggtcgt      1200
tgtttttcag cgaatccatt tgcgatcgct tttcaaaccc ttttttcgtc aaccttcttt      1260
aaacggcctc atgcatctcg cagttgtcgg ctcagccatc ggacagcacc gg              1312
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<210> 7

<211> 133

<212> DNA

<213> Nicotiana tabacum

<223> psbA promoter

<400> 7

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aagccttcca ttttctattt tgatttgtag aaaactagtg tgcttgggag tccctgatga      120
ttaaataaac caa                                                         133
```

<210> 8

<211> 159

<212> DNA

<213> Nicotiana tabacum

<223> rps16 terminator

<400> 8

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tatataactt tgtatgactt ttctcttcta tttttttgta tttcctccct ttccttttct      120
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<210> 9

<211> 805

<212> DNA

<213> Escherichia coli

<223> aadA

<400> 9

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tggatggcgg cctgaagcca cacagtgata ttgatttgct ggttacggtg accgtaaggc      180
ttgatgaaac aacgcggcga gctttgatca cgaccttttt ggaaacttcg gcttcccctg      240
gagagagcga gattctccgc gctgtagaag tcaccattgt tgtgcacgac gacatcattc      300
cgtggcgtta tccagctaag cgcgaactgc aatttggaga atggcagcgc aatgacattc      360
ttgcaggtat cttcgagcca gccacgatcg acattgatct ggctatcttg ctgacaaaag      420
caagagaaca tagcgttgcc ttggtaggtc cagcggcgga ggaactcttt gatccggttc      480
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actgggctgg cgatgagcga aatgtagtgc ttacgttgtc ccgcatttgg tacagcgcag      600
taaccggcaa aatcgcgccg aaggatgtcg ctgccgactg gcaatggag cgcctgccgg       660
cccagtatca gcccgtcata cttgaagcta gacaggctta tcttggacaa gaagaagatc      720
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<212> DNA
<213> Artificial sequence
<223> pLD6
<400> 10
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ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt     180
gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt     240
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aagcggaaga gcgcccaata cgcaaaccgc ctctccccgc gcgttggccg attcattaat     1980
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tgccagcgcc ctagcgcccg ctcctttcgc tttcttccct tcctttctcg ccacgttcgc     4260
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<213> Artificial sequence

<223> multi-cloning regions

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<211> 142

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<213> Nicotiana tabacum

<223> rrn promoter

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<213> Artificial sequence

<223> pLD200

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<211> 1434

<212> DNA

<213> Nicotiana tabacum

<223> rbcL

<400> 15

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<213> Nicotiana tabacum
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<213> Artificial sequence
<223> polylinker
<400> 17

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<210> 18
<211> 7
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<213> Artificial sequence
<223> Shine-Dalgarno Sequence
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